

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/523,038
Source: PT 10
Date Processed by STIC: 8/18/05

ENTERED

CRF Errors Edited by the STIC Systems Branch

Serial Number: 10523,038

CRF Edit Date: 8/22/05
Edited by: NS

___ Realigned nucleic acid/amino acid numbers/text in cases where the sequence text "wrapped" to the next line

___ Corrected the SEQ ID NO. Sequence numbers edited were:

___ Inserted or corrected a nucleic number at the end of a nucleic line. SEQ ID NO's edited:

___ Deleted: / invalid beginning/end-of-file text ; ___ page numbers

___ Inserted mandatory headings/numeric identifiers, specifically:

___ Moved responses to same line as heading/numeric identifier, specifically:

___ Other:



PCT10

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/523,038

DATE: 08/22/2005

TIME: 19:04:12

Input Set : A:\PTO.AMC.txt

Output Set: N:\CRF4\08222005\J523038.raw

3 <110> APPLICANT: SMITH, Harold
 4 SOWDEN, Mark P.
 5 DEWHURST, Stephen
 6 KIM, Baek
 7 WEDEKIND, Joseph
 9 <120> TITLE OF INVENTION: PROTEIN TRANSDUCING DOMAIN/DEAMINASE
 10 CHIMERIC PROTEINS, RELATED COMPOUNDS, AND USES THEREOF
 13 <130> FILE REFERENCE: 21108.0034U2
 15 <140> CURRENT APPLICATION NUMBER: 10/523,038
 C--> 16 <141> CURRENT FILING DATE: 2005-02-02
 18 <150> PRIOR APPLICATION NUMBER: PCT/US03/24458
 19 <151> PRIOR FILING DATE: 2003-08-05
 21 <150> PRIOR APPLICATION NUMBER: 60/419,982
 22 <151> PRIOR FILING DATE: 2002-10-21
 24 <150> PRIOR APPLICATION NUMBER: 60/401,293
 25 <151> PRIOR FILING DATE: 2002-08-05
 27 <160> NUMBER OF SEQ ID NOS: 49
 29 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 31 <210> SEQ ID NO: 1
 32 <211> LENGTH: 384
 33 <212> TYPE: PRT
 34 <213> ORGANISM: Artificial Sequence
 36 <220> FEATURE:
 37 <223> OTHER INFORMATION: Description of Artificial Sequence; note =
 38 synthetic construct
 40 <400> SEQUENCE: 1
 41 Met Lys Pro His Phe Arg Asn Thr Val Glu Arg Met Tyr Arg Asp Thr
 42 1 5 10 15
 43 Phe Ser Tyr Asn Phe Tyr Asn Arg Pro Ile Leu Ser Arg Arg Asn Thr
 44 20 25 30
 45 Val Trp Leu Cys Tyr Glu Val Lys Thr Lys Gly Pro Ser Arg Pro Pro
 46 35 40 45
 47 Leu Asp Ala Lys Ile Phe Arg Gly Gln Val Tyr Ser Glu Leu Lys Tyr
 48 50 55 60
 49 His Pro Glu Met Arg Phe Phe His Trp Phe Ser Lys Trp Arg Lys Leu
 50 65 70 75 80
 51 His Arg Asp Gln Glu Tyr Glu Val Thr Trp Tyr Ile Ser Trp Ser Pro
 52 85 90 95
 53 Cys Thr Lys Cys Thr Arg Asp Met Ala Thr Phe Leu Ala Glu Asp Pro
 54 100 105 110
 55 Lys Val Thr Leu Thr Ile Phe Val Ala Arg Leu Tyr Tyr Phe Trp Asp
 56 115 120 125
 57 Pro Asp Tyr Gln Glu Ala Leu Arg Ser Leu Cys Gln Lys Arg Asp Gly

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58      130      135      140
59 Pro Arg Ala Thr Met Lys Ile Met Asn Tyr Asp Glu Phe Gln His Cys
60 145      150      155      160
61 Trp Ser Lys Phe Val Tyr Ser Gln Arg Glu Leu Phe Glu Pro Trp Asn
62      165      170      175
63 Asn Leu Pro Lys Tyr Tyr Ile Leu Leu His Ile Met Leu Gly Glu Ile
64      180      185      190
65 Leu Arg His Ser Met Asp Pro Pro Thr Phe Thr Phe Asn Phe Asn Asn
66      195      200      205
67 Glu Pro Trp Val Arg Gly Arg His Glu Thr Tyr Leu Cys Tyr Glu Val
68      210      215      220
69 Glu Arg Met His Asn Asp Thr Trp Val Leu Leu Asn Gln Arg Arg Gly
70 225      230      235      240
71 Phe Leu Cys Asn Gln Ala Pro His Lys His Gly Phe Leu Glu Gly Arg
72      245      250      255
73 His Ala Glu Leu Cys Phe Leu Asp Val Ile Pro Phe Trp Lys Leu Asp
74      260      265      270
75 Leu Asp Gln Asp Tyr Arg Val Thr Cys Phe Thr Ser Trp Ser Pro Cys
76      275      280      285
77 Phe Ser Cys Ala Gln Glu Met Ala Lys Phe Ile Ser Lys Asn Lys His
78      290      295      300
79 Val Ser Leu Cys Ile Phe Thr Ala Arg Ile Tyr Asp Asp Gln Gly Arg
80 305      310      315      320
81 Cys Gln Glu Gly Leu Arg Thr Leu Ala Glu Ala Gly Ala Lys Ile Ser
82      325      330      335
83 Ile Met Thr Tyr Ser Glu Phe Lys His Cys Trp Asp Thr Phe Val Asp
84      340      345      350
85 His Gln Gly Cys Pro Phe Gln Pro Trp Asp Gly Leu Asp Glu His Ser
86      355      360      365
87 Gln Asp Leu Ser Gly Arg Leu Arg Ala Ile Leu Gln Asn Gln Glu Asn
88      370      375      380
90 <210> SEQ ID NO: 2
91 <211> LENGTH: 1155
92 <212> TYPE: DNA
93 <213> ORGANISM: Artificial Sequence
95 <220> FEATURE:
96 <223> OTHER INFORMATION: Description of Artificial Sequence; note =
97     synthetic construct
99 <400> SEQUENCE: 2
100 atgaagcctc acttcagaaa cacagtggag cgaatgtatc gagacacatt ctctacaac      60
101 ttttataata gaccatcct ttctcgtcgg aataccgtct ggctgtgcta cgaagtgaac      120
102 acaaagggtc cctcaaggcc ccctttggac gcaaagatct ttcgaggcca ggtgtattcc      180
103 gaacttaagt accaccaga gatgagattc ttccactggt tcagcaagtg gaggaagctg      240
104 catcgtgacc aggagtatga ggtcacctgg tacatatcct ggagcccctg cacaagtgt      300
105 acaagggtata tggccacgtt cctggccgag gaccgaagg ttaccctgac catcttcgtt      360
106 gccgcctct actacttctg ggaccagat taccaggagg cgcttcgcag cctgtgtcag      420
107 aaaagagacg gtccgcgtgc caccatgaag atcatgaatt atgacgaatt tcagcactgt      480
108 tggagcaagt tcgtgtacag ccaaagagag ctatttgagc cttggaataa tctgcctaaa      540
109 tattatatat tactgcacat catgctgggg gagattctca gacactcgat ggatccacc      600

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110 acattcactt tcaacttta caatgaacct tgggtcagag gacggcatga gacttacctg      660
111 tgttatgagg tggagcgcat gcacaatgac acctgggtcc tgctgaacca ggcagggggc      720
112 tttctatgca accaggctcc acataaacac ggtttccttg aaggccgcca tgcagagctg      780
113 tgcttcctgg acgtgattcc cttttggaag ctggacctgg accaggacta cagggttacc      840
114 tgcttcacct cctggagccc ctgcttcagc tgtgcccagg aaatggctaa attcatttca      900
115 aaaaacaaac acgtgagcct gtgcatcttc actgcccgcga tctatgatga tcaaggaaga      960
116 tgtcaggagg ggctgcgcac cctggccgag gctggggcca aaatttcaat aatgacatac     1020
117 agtgaattta agcactgctg ggacaccttt gtggaccacc agggatgtcc cttccagccc     1080
118 tgggatggac tagatgagca cagccaagac ctgagtggga ggctgcgggc cattctccag     1140
119 aatcaggaaa actga                                     1155
121 <210> SEQ ID NO: 3
122 <211> LENGTH: 198
123 <212> TYPE: PRT
124 <213> ORGANISM: Artificial Sequence
126 <220> FEATURE:
127 <223> OTHER INFORMATION: Description of Artificial Sequence; note =
128     synthetic construct
130 <400> SEQUENCE: 3
131 Met Asp Ser Leu Leu Met Asn Arg Arg Lys Phe Leu Tyr Gln Phe Lys
132 1          5          10          15
133 Asn Val Arg Trp Ala Lys Gly Arg Arg Glu Thr Tyr Leu Cys Tyr Val
134          20          25          30
135 Val Lys Arg Arg Asp Ser Ala Thr Ser Phe Ser Leu Asp Phe Gly Tyr
136          35          40          45
137 Leu Arg Asn Lys Asn Gly Cys His Val Glu Leu Leu Phe Leu Arg Tyr
138          50          55          60
139 Ile Ser Asp Trp Asp Leu Asp Pro Gly Arg Cys Tyr Arg Val Thr Trp
140 65          70          75          80
141 Phe Thr Ser Trp Ser Pro Cys Tyr Asp Cys Ala Arg His Val Ala Asp
142          85          90          95
143 Phe Leu Arg Gly Asn Pro Asn Leu Ser Leu Arg Ile Phe Thr Ala Arg
144          100         105         110
145 Leu Tyr Phe Cys Glu Asp Arg Lys Ala Glu Pro Glu Gly Leu Arg Arg
146          115         120         125
147 Leu His Arg Ala Gly Val Gln Ile Ala Ile Met Thr Phe Lys Asp Tyr
148          130         135         140
149 Phe Tyr Cys Trp Asn Thr Phe Val Glu Asn His Glu Arg Thr Phe Lys
150 145         150         155         160
151 Ala Trp Glu Gly Leu His Glu Asn Ser Val Arg Leu Ser Arg Gln Leu
152          165         170         175
153 Arg Arg Ile Leu Leu Pro Leu Tyr Glu Val Asp Asp Leu Arg Asp Ala
154          180         185         190
155 Phe Arg Thr Leu Gly Leu
156          195
158 <210> SEQ ID NO: 4
159 <211> LENGTH: 597
160 <212> TYPE: DNA
161 <213> ORGANISM: Artificial Sequence
163 <220> FEATURE:

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164 <223> OTHER INFORMATION: Description of Artificial Sequence; note =
165     synthetic construct
167 <400> SEQUENCE: 4
168 atggacagcc tcttgatgaa ccggaggaag tttctttacc aattcaaaaa tgtccgctgg      60
169 gctaagggtc ggcgtgagac ctacctgtgc tacgtagtga agaggcgtga cagtgtctaca      120
170 tcctttttcac tggacttttg ttatcttcgc aataagaacg gctgccacgt ggaattgctc      180
171 ttcctccgct acatctcgga ctgggacctt gacctggcc gctgctaccg cgtcacctgg      240
172 ttcacctcct ggagcccctg ctacgaactgt gcccgcacatg tggccgactt tctgcgaggg      300
173 aaccccaacc tcagtctgag gatcttcacc gcgcgcctct acttctgtga ggaccgcaag      360
174 gctgagcccg aggggctgcg gcggctgcac cgcccgggg tgcaaatagc catcatgacc      420
175 ttcaaagatt atttttactg ctggaatact tttgtagaaa accatgaaag aactttcaaa      480
176 gcctgggaag ggctgcatga aaattcagtt cgtctctcca gacagcttcg gcgcacacct      540
177 ttgcccctgt atgaggttga tgacttacga gacgcatttc gtactttggg actttga      597
179 <210> SEQ ID NO: 5
180 <211> LENGTH: 236
181 <212> TYPE: PRT
182 <213> ORGANISM: Artificial Sequence
184 <220> FEATURE:
185 <223> OTHER INFORMATION: Description of Artificial Sequence; note =
186     synthetic construct
188 <400> SEQUENCE: 5
189 Met Thr Ser Glu Lys Gly Pro Ser Thr Gly Asp Pro Thr Leu Arg Arg
190 1      5      10      15
191 Arg Ile Glu Pro Trp Glu Phe Asp Val Phe Tyr Asp Pro Arg Glu Leu
192      20      25      30
193 Arg Lys Glu Ala Cys Leu Leu Tyr Glu Ile Lys Trp Gly Met Ser Arg
194      35      40      45
195 Lys Ile Trp Arg Ser Ser Gly Lys Asn Thr Thr Asn His Val Glu Val
196      50      55      60
197 Asn Phe Ile Lys Lys Phe Thr Ser Glu Arg Asp Phe His Pro Ser Ile
198 65      70      75      80
199 Ser Cys Ser Ile Thr Trp Phe Leu Ser Trp Ser Pro Cys Trp Glu Cys
200      85      90      95
201 Ser Gln Ala Ile Arg Glu Phe Leu Ser Arg His Pro Gly Val Thr Leu
202      100     105     110
203 Val Ile Tyr Val Ala Arg Leu Phe Trp His Met Asp Gln Gln Asn Arg
204      115     120     125
205 Gln Gly Leu Arg Asp Leu Val Asn Ser Gly Val Thr Ile Gln Ile Met
206      130     135     140
207 Arg Ala Ser Glu Tyr Tyr His Cys Trp Arg Asn Phe Val Asn Tyr Pro
208 145     150     155     160
209 Pro Gly Asp Glu Ala His Trp Pro Gln Tyr Pro Pro Leu Trp Met Met
210      165     170     175
211 Leu Tyr Ala Leu Glu Leu His Cys Ile Ile Leu Ser Leu Pro Pro Cys
212      180     185     190
213 Leu Lys Ile Ser Arg Arg Trp Gln Asn His Leu Thr Phe Phe Arg Leu
214      195     200     205
215 His Leu Gln Asn Cys His Tyr Gln Thr Ile Pro Pro His Ile Leu Leu
216      210     215     220

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217 Ala Thr Gly Leu Ile His Pro Ser Val Ala Trp Arg
 218 225 230 235

220 <210> SEQ ID NO: 6

221 <211> LENGTH: 863

222 <212> TYPE: DNA

223 <213> ORGANISM: Artificial Sequence

225 <220> FEATURE:

226 <223> OTHER INFORMATION: Description of Artificial Sequence; note =

227 synthetic construct

229 <400> SEQUENCE: 6

230	gatcccagag	gaggaagtcc	agagacagag	caccatgact	tctgagaaag	gagaagaatc	60
231	gaaccctggg	agtttgacgt	cttctatgac	cccagagaac	ttcgtaaaga	ggcctgtctg	120
232	ctctacgaaa	tcaagtgggg	catgagccgg	aagatctggc	gaagctcagg	caaaaacacc	180
233	accaatcacg	tggaagttaa	ttttataaaa	aaatttacgt	cagaaagaga	ttttcaccca	240
234	tccatcacgt	gctccatcac	ctggttcttg	tcctggagtc	cctgctggga	atgctcccag	300
235	gctattagag	agtttctgag	tcggcaccct	ggtgtgactc	tagtgatcta	cgtagctcgg	360
236	cttttttggc	acatggatca	acaaaatcgg	caagggtctca	gggaccttgt	taacagtgga	420
237	gtaactattc	agattatgag	agcatcagag	tattatcact	gctggaggaa	ttttgtcaac	480
238	taccacacctg	gggatgaagc	tcactggcca	caatacccac	ctctgtggat	gatgtgttac	540
239	gcactggagc	tgcactgcat	aattctaagt	cttccaccct	gtttaaagat	ttcaagaaga	600
240	tggcaaaatc	atcttacatt	tttcagactt	catcttcaaa	actgccatta	ccaaacgatt	660
241	ccgccacaca	tcctttttagc	tacagggctg	atacatcctt	ctgtggcttg	gagatgaata	720
242	ggatgattcc	gtgtgtgtac	tgattcaaga	acaagcaatg	atgaccctact	aaagagtga	780
243	tgccatttag	aatctagaaa	tgttcacaa	gtaccccaaa	actctgtagc	ttaaaccaac	840
244	aataaatatg	tattacctct	ggc				863

247 <210> SEQ ID NO: 7

248 <211> LENGTH: 192

249 <212> TYPE: PRT

250 <213> ORGANISM: Artificial Sequence

252 <220> FEATURE:

253 <223> OTHER INFORMATION: Description of Artificial Sequence; note =

254 synthetic construct

256 <400> SEQUENCE: 7

257	Met	Glu	Asn	Arg	Trp	Gln	Val	Met	Ile	Val	Trp	Gln	Val	Asp	Arg	Met
258	1			5					10					15		
259	Arg	Ile	Lys	Thr	Trp	Lys	Ser	Leu	Val	Lys	His	His	Met	Tyr	Ile	Ser
260				20				25						30		
261	Lys	Lys	Ala	Lys	Glu	Trp	Val	Tyr	Arg	His	His	Tyr	Glu	Ser	Thr	His
262			35				40						45			
263	Pro	Arg	Ile	Ser	Ser	Glu	Val	His	Ile	Pro	Leu	Gly	Asp	Ala	Lys	Leu
264		50				55					60					
265	Val	Ile	Thr	Thr	Tyr	Trp	Gly	Leu	His	Thr	Gly	Glu	Arg	Glu	Trp	His
266	65				70			75						80		
267	Leu	Gly	Gln	Gly	Val	Ser	Ile	Glu	Trp	Arg	Lys	Lys	Arg	Tyr	Asn	Thr
268			85			90								95		
269	Gln	Val	Asp	Pro	Asp	Leu	Ala	Asp	Lys	Leu	Ile	His	Leu	His	Tyr	Phe
270			100			105							110			
271	Asp	Cys	Phe	Ser	Asp	Ser	Ala	Ile	Arg	His	Ala	Ile	Leu	Gly	His	Arg
272			115			120							125			

VERIFICATION SUMMARY

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L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date